

I

SID 1 - 100% hit

RESULT 1  
D84401  
LOCUS D84401 42398 bp DNA PRI 20-NOV-1999  
DEFINITION Homo sapiens genomic DNA, 43 kb segment from chromosome6, complete sequence.  
ACCESSION D84401  
VERSION D84401.1 GI:2401263  
KEYWORDS HTG.  
SOURCE Homo sapiens cell\_line:CGMI DNA, clone:519.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Kikuti,Y.Y., Tamiya,G., Ando,A., Chen,L., Kimura,M., Ferreira,E., Tsuji,K., Trowsdale,J. and Inoko,H.  
TITLE Physical mapping 220 kb centromeric of the human MHC and DNA sequence analysis of the 43-kb segment including the RING1, HKE6, and HKE4 genes  
JOURNAL Genomics 42 (3), 422-435 (1997)  
MEDLINE 97349110  
REFERENCE 2 (bases 1 to 42398)  
AUTHORS Kikuti,Y., Inoko,H., Ando,A., Kimura,M., Watanabe,K. and Shiina,T.  
TITLE Physical map of 200 kb at the centromeric side of the human MHC region and sequence of 43 kb  
JOURNAL Unpublished (1996)  
REFERENCE 3 (bases 1 to 42398)  
AUTHORS Inoko,H.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-1996) to the DDBJ/EMBL/GenBank databases.  
Hidetoshi Inoko, Tokai University School of Medicine, Molecular Life Science; Bohseidai, Isehara, Kanagawa 259-11, Japan (E-mail:hinoko@is.icc.u-tokai.ac.jp, Tel:0463-93-1121, Fax:0463-94-8884)  
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ORIGIN

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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LOCUS HS1033B10 175737 bp DNA PRI 11-MAY-2001

SID 2 13,194-13,175

419  
42052

DEFINITION Human DNA sequence from clone RP5-1033B10 on chromosome 6p21.2-21.31 Contains the D6S2723E gene for DNA segment on chromosome 6 (unique, pseudogene) 2723 expressed sequence (BING5), the gene C6ORF11 for chromosome 6 open reading frame 11 (BING4), the B3GALT4 gene for UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase polypeptide 4, the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a HTATSF1 (HIV TAT specific factor 1) pseudogene, a pseudogene similar to zinc finger genes, the RING1 gene for ring finger protein 1, the FABGL gene for FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like protein, the HKE4 gene for HLA class II region expressed gene KE4, the RXRB (retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, a pseudogene similar to HLA DPA1 antigen, part of a pseudogene similar to HLA class II histocompatibility antigen, DP beta chain precursors (HLA-DPB2), a putative novel gene, seve>.

ACCESSION AL031228

VERSION AL031228.1 GI:3646023

KEYWORDS HTG; acyl-carrier-protein; B3GALT4; beta3-Galactosyltransferase; BING4; BING5; C6ORF11; COL11A2; collagen; CpG island; D6S2723E; F28D1.1; FABGL; HKE4; HKE6; HLA-DPA3; HLA-DPB2; KE4; retinoid X receptor beta; ribosomal protein; ring finger; RING1; RING2; RING5; RPS18; RXRB; SACM2L; short-chain alcohol dehydrogenase; zinc finger.

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 175737)

AUTHORS Tubby,B.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Sep 24, 1998 this sequence version replaced gi:3550015. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>  
 RP5-1033B10 is from the library RPCI-5 constructed by the group of  
 Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pCYPAC2

This sequence is the entire insert of clone RP5-1033B10.

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repeat_region	63. .368 /note="AluSx repeat: matches 1. .299 of consensus"
repeat_region	374. .403 /note="Cheshire repeat: matches 2264. .2292 of consensus"
repeat_region	404. .708 /note="AluSq repeat: matches 1. .305 of consensus"
repeat_region	719. .1027 /note="AluJb repeat: matches 1. .303 of consensus"
repeat_region	1028. .1220 /note="Cheshire repeat: matches 2055. .2256 of consensus"
repeat_region	1227. .1583 /note="Cheshire repeat: matches 1. .376 of consensus"
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CDS	complement(1534. .1961) /gene="D6S2723E" /note="dJ1033B10.1 (DNA segment on chromosome 6 (unique, pseudogene) 2723 expressed sequence (BING5)) overlaps cICF0811 match: ESTs: Em:AW379285 match: proteins: Tr:O15214" /codon_start=1 /pseudo /evidence=not_experimental
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repeat_region	1962. .2265 /note="AluSg repeat: matches 1. .296 of consensus"
repeat_region	2305. .2609 /note="AluSx repeat: matches 1. .307 of consensus"
repeat_region	2749. .2926 /note="AluJb repeat: matches 1. .165 of consensus"
repeat_region	3009. .3297 /note="AluSg repeat: matches 1. .290 of consensus"
repeat_region	4125. .4385 /note="AluSx repeat: matches 20. .294 of consensus"
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 AEKHCPMARYVLKTDVVYVNPVELVSELVLRGGRWGQWERSTEPQREAEQEGGQVLH  
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Query Match 100.0%; Score 19; DB 9; Length 175737;  
 Best Local Similarity 100.0%; Pred. No. 16;  
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RESULT 3  
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 DEFINITION Homo sapiens chromosome 18 clone RP11-602P21 map 18, WORKING DRAFT  
 SEQUENCE, 49 unordered pieces.  
 ACCESSION AC040962  
 VERSION AC040962.2 GI:7960461  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 200548)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 TITLE Homo sapiens chromosome 18, clone RP11-602P21  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 200548)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,  
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 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Direct Submission  
 Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 21, 2000 this sequence version replaced gi:7534164.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L9240  
 Center clone name: 602\_P\_21

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 177125 bases at least Q40  
 Consensus quality: 187777 bases at least Q30  
 Consensus quality: 192419 bases at least Q20  
 Insert size: 205000; agarose-fp  
 Insert size: 195748; sum-of-contigs  
 Quality coverage: 3.6 in Q20 bases; agarose-fp  
 Quality coverage: 3.7 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 49 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 1046: contig of 1046 bp in length  
 \* 1047 1146: gap of 100 bp  
 \* 1147 2330: contig of 1184 bp in length

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* 83481 83580: gap of 100 bp
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* 88261 88360: gap of 100 bp
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* 121429 121528: gap of 100 bp
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* 143541 143640: gap of 100 bp
* 143641 151858: contig of 8218 bp in length
* 151859 151958: gap of 100 bp
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* 161624 161723: gap of 100 bp
* 161724 172118: contig of 10395 bp in length
* 172119 172218: gap of 100 bp
* 172219 180457: contig of 8239 bp in length
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* 190269 190368: gap of 100 bp
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Query Match 100.0%; Score 19; DB 2; Length 200548;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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